



Warf Sequence.ST25.txt
SEQUENCE LISTING

<110> Harms, Jerome S
Splitter, Gary A
Eakle, Kurt A
Bremel, Robert D

<120> Inducible Protein Expression System

<130> 2240/3

<140> US 10/763,976

<141> 2004-01-23

<160> 65

<170> PatentIn version 3.3

<210> 1

<211> 576

<212> DNA

<213> Artificial

<220>

<223> Engineered Sequence from virus and plasmid

<220>

<221> Promoter

<222> (87)..(432)

<223> BLV Promoter

<400> 1

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aattacaact gctagaaaat gaatggctct cccgcctttt ttgaggggga atcatttgta	180
tgaaagatca tgccgaccta ggcgccgcca ccgccccgta aaccagacag agacgtcagc	240
tgccagaaaa gctggtgacg gcagctgggtg gctagaatcc ccgtacctcc ccaacttccc	300
ctttcccga aaatccacac cctgagctgc tgacctcacc tgctgataaa ttaataaaat	360
gccggccctg tcgagttagc ggcaccagaa gcgttcttct cctgagacct tcgtgctcag	420
ctctcgttcc tgcctcgaga agcttggtat cacaagtttg tacaaaaaag ctgaacgaga	480
aacgtaaaat gatataaata tcaatatatt aaattagatt ttgcataaaa aacagactac	540
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<210> 2

<211> 930

<212> DNA

<213> Bovine leukemia virus

<220>

<221> CDS

<222> (1)..(930)

Warf Sequence.ST25.txt

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<400> 2
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Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
1 5 10 15

gcc ctg gtt ttg tcc aat gac gtc acc atc gat gcc tgg tgc ccc ctc      96
Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
20 25 30

tgc ggg ccc cat gag cga ctc caa ttc gaa agg atc gac acc acg cac      144
Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
35 40 45

acc tgc gag acc cac cgt atc acc tgg acc gcc gat gga cga cct ttc      192
Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
50 55 60

ggc ctc aat gga gcg ctg ttc cct cga ctg cat gtc tcc aga gac ccg      240
Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
65 70 75 80

gcc cca agg gcc cga cga ctc tgg atc aac tgc ccc ctt ccg gcc gtt      288
Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
85 90 95

cgc gct cag ccc ggc ccg gtt tca ctt tcc ccc ttc gag cgg tcc ccc      336
Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
100 105 110

ttc cag ccc tac caa tgc caa ttg ccc tcg gcc tct agc gac ggt tgc      384
Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
115 120 125

ccc gtc atc ggg cac ggc ctt ctt ccc tgg aac aac tta gta acg cat      432
Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
130 135 140

cct tgt cct cgg aaa gtc ctt ata tta aat caa atg gcc aat ttt tcc      480
Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
145 150 155 160

tta ctc ccc ccc ttc aat acc ctc ctt gtg gac ccc ctc cgg ttg tcc      528
Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
165 170 175

gtc ttt gcc cca gac acc agg gga gcc ata cgt tat ctc tcc acc ctt      576
Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
180 185 190

ttg acg cta tgc cca gct act tgt att cta ccc ctc ggc gag ccc ttc      624
Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
195 200 205

tct cct aat gtc ccc ata tgt cgc ttt ccc cgg gac tcc aat gaa ccc      672
Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
210 215 220

ccc ctt tca gaa ttc gag ctg ccc ctt atc caa acg ccc ggc ctg tct      720
Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
225 230 235 240

tgg tct gtc ccc gcg atc gac cta ttc cta acc ggc ccc cct tcc cca      768

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Warf Sequence.ST25.txt

Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
245 250 255

tgc gac cgg tta cac gta tgg tcc agt cct cag gcc tta cag cgc ttc 816
Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
260 265 270

ctc cat gac cct acg cta acc tgg tca gaa ttg gtt gct agc agg aaa 864
Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
275 280 285

cta aga ctt gat tca ccc tta aaa tta caa ctg tta gaa aat gaa tgg 912
Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
290 295 300

ctc tcc cgc ctt ttt tga 930
Leu Ser Arg Leu Phe
305

<210> 3
<211> 309
<212> PRT
<213> Bovine leukemia virus

<400> 3

Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
1 5 10 15

Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
20 25 30

Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
35 40 45

Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
50 55 60

Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
65 70 75 80

Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
85 90 95

Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
100 105 110

Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
115 120 125

Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
130 135 140

warf Sequence.ST25.txt

Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
145 150 155 160

Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
165 170 175

Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
180 185 190

Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
195 200 205

Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
210 215 220

Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
225 230 235 240

Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
245 250 255

Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
260 265 270

Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
275 280 285

Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
290 295 300

Leu Ser Arg Leu Phe
305

<210> 4
<211> 1062
<212> DNA
<213> Human T-cell lymphotropic virus type 1

<220>
<221> promoter
<222> (1)..(353)

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catcgtcacg ccctactggc cacctgtcca gagcatcaga tcacctggga ccccatcgat 180
ggacgcgtta tcggctcagc tctacagttc cttatccctc gactccctc cttccccacc 240

warf Sequence.ST25.txt

cagagaacct ctaagaccct caaggctcctt accccgccaa tcactcatac aacccccaac 300
attccaccct ccttcctcca ggccatgcgc aaatactccc ccttccgaaa tggatacatg 360
gaaccacccc ttgggcagca cctcccaacc ctgtcttttc cagaccccg g actccggccc 420
caaaacctgt acaccctctg gggaggctcc gttgtctgca tgtacctcta ccagctttcc 480
ccccccatca cctggcccct cctgccccac gtgatttttt gccaccccg g ccagctcggg 540
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accacagggg ccctaataat tctacccgaa gactgtttgc ccaccaccct tttccagcct 660
gttagggcac ccgtcacgct aacagcctgg caaaacggcc tccttccggt ccactcaacc 720
ctcaccactc caggccttat ttggacattt accgatggca cgcctatgat ttccgggccc 780
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tttcaaacca aggcctacca cccctcattt ctactctcac acggcctcat acagtactct 900
tcctttcata atttacatct cctgtttgaa gaatacacca acatccccat ttctctactt 960
tttaacaaaa aagaggcaga tgacaatgac catgagcccc aaatatcccc cgggggctta 1020
gagcctccca gtgaaaaaca tttccgcgaa acagaagtct ga 1062

<210> 5
<211> 353
<212> DNA
<213> Human T-cell lymphotropic virus type 1

<400> 5
tgacaatgac catgagcccc aaatatcccc cgggggctta gagcctctca gtgaaaaaca 60
tttccgtgaa acagaagtct gagaaggctca gggcccagaa taaggctctg acgtctcccc 120
ccggaggaca gctcagcacc agctcaggct aggccttgac gtgtccccct aaagacaaat 180
cataagctca gacctccggg aagccaccgg gaaccaccca tttcctcccc atgtttgtca 240
agccgtcctc aggcgttgac gacaaccctt cacctcaaaa aacttttcat ggcacgcata 300
cggtcaata aaataacagg agtctataaa agcgtgggga cagttcagga ggg 353

<210> 6
<211> 456
<212> DNA
<213> Human immunodeficiency virus type 1

<220>
<221> CDS
<222> (1)..(456)

<400> 6
ctg gaa ggg cta att tgg tcc caa aga aga caa gag atc ctt gat ctg 48
Leu Glu Gly Leu Ile Trp Ser Gln Arg Arg Gln Glu Ile Leu Asp Leu
1 5 10 15

warf Sequence.ST25.txt

tgg atc tac cac aca caa ggc tac ttc cct gat tgg cag aat tac aca	96
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr	
20 25 30	
cca ggg cca ggg atc aga tat cca ctg acc ttt gga tgg tgc ttc aag	144
Pro Gly Pro Gly Ile Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe Lys	
35 40 45	
cta gta cca gtt gag cca gag aag gta gaa gag gcc aat gaa gga gag	192
Leu Val Pro Val Glu Pro Glu Lys Val Glu Glu Ala Asn Glu Gly Glu	
50 55 60	
aac aac agc ttg tta cac cct atg agc ctg cat ggg atg gag gac gcg	240
Asn Asn Ser Leu Leu His Pro Met Ser Leu His Gly Met Glu Asp Ala	
65 70 75 80	
gag aaa gaa gtg tta gtg tgg agg ttt gac agc aaa cta gca ttt cat	288
Glu Lys Glu Val Leu Val Trp Arg Phe Asp Ser Lys Leu Ala Phe His	
85 90 95	
cac atg gcc cga gag ctg cat ccg gag tac tac aaa gac tgc tga cat	336
His Met Ala Arg Glu Leu His Pro Glu Tyr Tyr Lys Asp Cys His	
100 105 110	
cga gct ttc tac aag gga ctt tcc gct ggg gac ttt cca ggg agg cgt	384
Arg Ala Phe Tyr Lys Gly Leu Ser Ala Gly Asp Phe Pro Gly Arg Arg	
115 120 125	
ggc ctg ggc ggg act ggg gag tgg cgt ccc tca gat gct gca tat aag	432
Gly Leu Gly Gly Thr Gly Glu Trp Arg Pro Ser Asp Ala Ala Tyr Lys	
130 135 140	
cag ctg ctt ttt gcc tgt act ggg	456
Gln Leu Leu Phe Ala Cys Thr Gly	
145 150	

<210> 7
 <211> 110
 <212> PRT
 <213> Human immunodeficiency virus type 1

<400> 7

Leu Glu Gly Leu Ile Trp Ser Gln Arg Arg Gln Glu Ile Leu Asp Leu
 1 5 10 15

Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
 20 25 30

Pro Gly Pro Gly Ile Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe Lys
 35 40 45

Leu Val Pro Val Glu Pro Glu Lys Val Glu Glu Ala Asn Glu Gly Glu
 50 55 60

Asn Asn Ser Leu Leu His Pro Met Ser Leu His Gly Met Glu Asp Ala
 65 70 75 80

Warf Sequence.ST25.txt

Glu Lys Glu Val Leu Val Trp Arg Phe Asp Ser Lys Leu Ala Phe His
85 90 95

His Met Ala Arg Glu Leu His Pro Glu Tyr Tyr Lys Asp Cys
100 105 110

<210> 8
<211> 41
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 8

His Arg Ala Phe Tyr Lys Gly Leu Ser Ala Gly Asp Phe Pro Gly Arg
1 5 10 15

Arg Gly Leu Gly Gly Thr Gly Glu Trp Arg Pro Ser Asp Ala Ala Tyr
20 25 30

Lys Gln Leu Leu Phe Ala Cys Thr Gly
35 40

<210> 9
<211> 306
<212> DNA
<213> Human immunodeficiency virus type 1

<220>
<221> CDS
<222> (1)..(303)

<400> 9

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Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

cag cct agg act gct tgt aac aat tgc tat tgt aaa aag tgt tgc ttt 96
Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

cat tgc tac gcg tgt ttc aca aga aaa ggc tta ggc atc tcc tat ggc 144
His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile Ser Tyr Gly
35 40 45

agg aag aag cgg aga cag cga aga gct cct cag gac agt cag act 192
Arg Lys Lys Arg Arg Gln Arg Arg Ala Pro Gln Asp Ser Gln Thr
50 55 60

cat caa gct tct cta tca aag caa ccc gcc tcc cag tcc cga ggg gac 240
His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser Gln Ser Arg Gly Asp
65 70 75 80

ccg aca ggc ccg acg gaa tcg aag aag aag gtg gag aga gag aca gag 288
Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys Val Glu Arg Glu Thr Glu
85 90 95

aca gat ccg ttc gat tag
Thr Asp Pro Phe Asp
100

<210> 10
<211> 101
<212> PRT
<213> Human immunodeficiency virus type 1
<400> 10

Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile Ser Tyr Gly
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln Asp Ser Gln Thr
50 55 60

His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser Gln Ser Arg Gly Asp
65 70 75 80

Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys Val Glu Arg Glu Thr Glu
85 90 95

Thr Asp Pro Phe Asp
100

<210> 11
<211> 309
<212> PRT
<213> Bovine leukemia virus
<400> 11

Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
1 5 10 15

Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
20 25 30

Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
35 40 45

Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
50 55 60

Warf Sequence.ST25.txt

Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
 65 70 75 80
 Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
 85 90 95
 Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
 100 105 110
 Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
 115 120 125
 Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
 130 135 140
 Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
 145 150 155 160
 Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
 165 170 175
 Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
 180 185 190
 Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
 195 200 205
 Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
 210 215 220
 Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
 225 230 235 240
 Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
 245 250 255
 Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
 260 265 270
 Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
 275 280 285
 Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
 290 295 300
 Leu Ser Arg Leu Phe
 305

warf Sequence.ST25.txt

<210> 12
 <211> 353
 <212> PRT
 <213> Human T-cell lymphotropic virus type 1

<400> 12

Met Ala His Phe Pro Gly Phe Gly Gln Ser Leu Leu Phe Gly Tyr Pro
 1 5 10 15

Val Tyr Val Phe Gly Asp Cys Val Gln Gly Asp Trp Cys Pro Ile Ser
 20 25 30

Gly Gly Leu Cys Ser Ala Arg Leu His Arg His Ala Leu Leu Ala Thr
 35 40 45

Cys Pro Glu His Gln Ile Thr Trp Asp Pro Ile Asp Gly Arg Val Ile
 50 55 60

Gly Ser Ala Leu Gln Phe Leu Ile Pro Arg Leu Pro Ser Phe Pro Thr
 65 70 75 80

Gln Arg Thr Ser Lys Thr Leu Lys Val Leu Thr Pro Pro Ile Thr His
 85 90 95

Thr Thr Pro Asn Ile Pro Pro Ser Phe Leu Gln Ala Met Arg Lys Tyr
 100 105 110

Ser Pro Phe Arg Asn Gly Tyr Met Glu Pro Thr Leu Gly Gln His Leu
 115 120 125

Pro Thr Leu Ser Phe Pro Asp Pro Gly Leu Arg Pro Gln Asn Leu Tyr
 130 135 140

Thr Leu Trp Gly Gly Ser Val Val Cys Met Tyr Leu Tyr Gln Leu Ser
 145 150 155 160

Pro Pro Ile Thr Trp Pro Leu Leu Pro His Val Ile Phe Cys His Pro
 165 170 175

Gly Gln Leu Gly Ala Phe Leu Thr Asn Val Pro Tyr Lys Arg Ile Glu
 180 185 190

Glu Leu Leu Tyr Lys Ile Ser Leu Thr Thr Gly Ala Leu Ile Ile Leu
 195 200 205

Pro Glu Asp Cys Leu Pro Thr Thr Leu Phe Gln Pro Val Arg Ala Pro
 210 215 220

warf Sequence.ST25.txt

Val Thr Leu Thr Ala Trp Gln Asn Gly Leu Leu Pro Phe His Ser Thr
 225 230 235 240
 Leu Thr Thr Pro Gly Leu Ile Trp Thr Phe Thr Asp Gly Thr Pro Met
 245 250 255
 Ile Ser Gly Pro Cys Pro Lys Asp Gly Gln Pro Ser Leu Val Leu Gln
 260 265 270
 Ser Ser Ser Phe Ile Phe His Lys Phe Gln Thr Lys Ala Tyr His Pro
 275 280 285
 Ser Phe Leu Leu Ser His Gly Leu Ile Gln Tyr Ser Ser Phe His Asn
 290 295 300
 Leu His Leu Leu Phe Glu Glu Tyr Thr Asn Ile Pro Ile Ser Leu Leu
 305 310 315 320
 Phe Asn Lys Lys Glu Ala Asp Asp Asn Asp His Glu Pro Gln Ile Ser
 325 330 335
 Pro Gly Gly Leu Glu Pro Pro Ser Glu Lys His Phe Arg Glu Thr Glu
 340 345 350

Val

<210> 13
 <211> 101
 <212> PRT
 <213> Human T-cell lymphotropic virus type 1
 <400> 13

Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly Ser
 1 5 10 15
 Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys Cys Phe
 20 25 30
 His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile Ser Tyr Gly
 35 40 45
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln Asp Ser Gln Thr
 50 55 60
 His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser Gln Ser Arg Gly Asp
 65 70 75 80

Warf Sequence.ST25.txt

Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys Val Glu Arg Glu Thr Glu
85 90 95

Thr Asp Pro Phe Asp
100

<210> 14
<211> 7685
<212> DNA
<213> Artificial

<220>
<223> Engineered Sequence from virus and plasmid

<220>
<221> LTR
<222> (149)..(737)
<223> 5' MoMuSVLTR

<220>
<221> CDS
<222> (1753)..(2148)
<223> Blasticidin Resistance

<220>
<221> promoter
<222> (2257)..(3074)
<223> CMV IE promoter

<220>
<221> misc_recomb
<222> (3078)..(3102)
<223> attB1

<220>
<221> CDS
<222> (3115)..(4041)
<223> BLV Tax

<220>
<221> misc_recomb
<222> (4046)..(4070)
<223> attB2

<220>
<221> misc_signal
<222> (4082)..(4674)
<223> WPRE; woodchuck hepatitis virus post-transcriptional regulatory element

<220>
<221> LTR
<222> (4720)..(5313)
<223> 3' MoMuLVLTR

<220>
<221> CDS
<222> (6616)..(7476)
<223> Ampicillin Resistance

Warf Sequence.ST25.txt

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<400> 14
gaattaattc ataccagatc accgaaaact gtcctccaaa tgtgtccccc tcacactccc      60
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aaagccgcgg cccttccggt tctttgcttt tgaaagaccc cacccgtagg tggcaagcta      180
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agatcaaggt caggaacaaa gaaacagctg aataccaaac aggatatctg tggtaagcgg      300
ttcctgcccc ggctcagggc caagaacaga tgagacagct gagtgatggg ccaaacagga      360
tatctgtggt aagcagttcc tgccccggct cggggccaag aacagatggg cccagatgc      420
gggtccagccc tcagcagttt ctagtgaatc atcagatggt tccaggggtgc cccaaggacc      480
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cttccgatag actgcgtcgc ccgggtaccc gtattcccaa taaagcctct tgctgtttgc      660
atccgaatcg tgggtctcgt gttccttggg aggggtctcct ctgagtgatt gactaccac      720
gacgggggtc tttcatttgg gggctcgtcc gggatttggg gaccctgcc cagggaccac      780
cgaccacca ccgggaggta agctggccag caacttatct gtgtctgtcc gattgtctag      840
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cgtctgaatt tttgctttcg gtttggaaac gaagccgcgc gtcttgtctg ctgcagcgtc     1140
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gccagactgt taccactccc ttaagtttga ccttaggtca ctggaaagat gtcgagcggg     1260
tcgctcacia ccagtcggta gatgtcaaga agagacgttg ggttaccttc tgctctgcag     1320
aatggccaac ctttaacgtc ggatggccgc gagacggcac ctttaaccga gacctcatca     1380
cccagggtta gatcaaggtc tttcacctg gcccgcattg acaccagac cagggtcccct     1440
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accctaagcc tccgcctcct ctctctccat ccgccccgtc tctccccctt gaacctcctc     1560
gttcgacccc gcctcgatcc tccctttatc cagccctcac tccttctcta ggcgccggaa     1620
ttccgatctg atcaagagac aggatgaggg agcttgata tccattttcg gatctgatca     1680
gcacgtgttg acaattaatc atcggcatag tatatcggca tagtataata cgacaaggtg     1740
aggaactaaa cc atg gcc aag cct ttg tct caa gaa gaa tcc acc ctc att     1791
                1      5      10
                Met Ala Lys Pro Leu Ser Gln Glu Glu Ser Thr Leu Ile

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warf Sequence.ST25.txt

gaa aga gca acg gct aca atc aac agc atc ccc atc tct gaa gac tac Glu Arg Ala Thr Ala Thr Ile Asn Ser Ile Pro Ile Ser Glu Asp Tyr 15 20 25	1839
agc gtc gcc agc gca gct ctc tct agc gac ggc cgc atc ttc act ggt Ser Val Ala Ser Ala Ala Leu Ser Ser Asp Gly Arg Ile Phe Thr Gly 30 35 40 45	1887
gtc aat gta tat cat ttt act ggg gga cct tgt gca gaa ctc gtg gtg Val Asn Val Tyr His Phe Thr Gly Gly Pro Cys Ala Glu Leu Val Val 50 55 60	1935
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gcg atc gga aat gag aac agg ggc atc ttg agc ccc tgc gga cgg tgt Ala Ile Gly Asn Glu Asn Arg Gly Ile Leu Ser Pro Cys Gly Arg Cys 80 85 90	2031
cga cag gtg ctt ctc gat ctg cat cct ggg atc aaa gcg ata gtg aag Arg Gln Val Leu Leu Asp Leu His Pro Gly Ile Lys Ala Ile Val Lys 95 100 105	2079
gac agt gat gga cag ccg acg gca gtt ggg att cgt gaa ttg ctg ccc Asp Ser Asp Gly Gln Pro Thr Ala Val Gly Ile Arg Glu Leu Leu Pro 110 115 120 125	2127
tct ggt tat gtg tgg gag ggc taagcacttc gtggccgagg agcaggactg Ser Gly Tyr Val Trp Glu Gly 130	2178
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cgttttccgg gacgccgatc cggccattag ccatattatt cattggttat atagcataaa	2298
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warf Sequence.ST25.txt

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Trp	Gly	Pro	His	Ser	Leu	His	Ala	Cys	Pro	Ala	Leu	Val	Leu	Ser	Asn	
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Asp	Val	Thr	Ile	Asp	Ala	Trp	Cys	Pro	Leu	Cys	Gly	Pro	His	Glu	Arg	
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Leu	Gln	Phe	Glu	Arg	Ile	Asp	Thr	Thr	Leu	Thr	Cys	Glu	Thr	His	Arg	
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atc	aac	tgg	acc	gcc	gat	gga	cga	cct	tgc	ggc	ctc	aat	gga	acg	ttg	3324
Ile	Asn	Trp	Thr	Ala	Asp	Gly	Arg	Pro	Cys	Gly	Leu	Asn	Gly	Thr	Leu	
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Phe	Pro	Arg	Leu	His	Val	Ser	Glu	Thr	Arg	Pro	Gln	Gly	Pro	Arg	Arg	
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ctc	tgg	atc	aac	tgc	ccc	ctt	ccg	gcc	gtt	cgc	gct	cag	ccc	ggc	ccg	3420
Leu	Trp	Ile	Asn	Cys	Pro	Leu	Pro	Ala	Val	Arg	Ala	Gln	Pro	Gly	Pro	
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gtt	tca	ctt	tcc	ccc	ttc	gag	cgg	tcc	ccc	ttc	cag	ccc	tac	caa	tgc	3468
Val	Ser	Leu	Ser	Pro	Phe	Glu	Arg	Ser	Pro	Phe	Gln	Pro	Tyr	Gln	Cys	
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Gln	Leu	Pro	Ser	Ala	Ser	Ser	Asp	Gly	Cys	Pro	Ile	Ile	Gly	His	Gly	
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Leu	Leu	Pro	Trp	Asn	Asn	Leu	Val	Thr	His	Pro	Val	Leu	Arg	Lys	Val	
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acc	ctc	ctt	gtg	gac	ccc	ctc	cgg	ctg	tcc	gtc	ttt	gcc	cca	gac	acc	3660
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Arg	Gly	Ala	Ile	Arg	Tyr	Leu	Ser	Thr	Leu	Leu	Thr	Leu	Cys	Pro	Ala	
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act	tgt	att	cta	ccc	cta	ggc	gag	ccc	ttc	tct	cct	aat	gtc	ccc	ata	3756
Thr	Cys	Ile	Leu	Pro	Leu	Gly	Glu	Pro	Phe	Ser	Pro	Asn	Val	Pro	Ile	
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Cys	Arg	Phe	Pro	Arg	Asp	Ser	Asn	Glu	Pro	Pro	Leu	Ser	Glu	Phe	Glu	
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ctg	ccc	ctt	atc	caa	acg	ccc	ggc	ctg	tct	tgg	tct	gtc	ccc	gcg	atc	3852
Leu	Pro	Leu	Ile	Gln	Thr	Pro	Gly	Leu	Ser	Trp	Ser	Val	Pro	Ala	Ile	
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warf Sequence.ST25.txt

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tgg tcc agt cct cag gcc tta cag cgc ttc ctt cat gac cct acg cta Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe Leu His Asp Pro Thr Leu 395 400 405 410	3948
acc tgg tcc gaa tta gtt gct agc aga aaa ata aga ctt gat tcc ccc Thr Trp Ser Glu Leu Val Ala Ser Arg Lys Ile Arg Leu Asp Ser Pro 415 420 425	3996
tta aaa tta caa ctg cta gaa aat gaa tgg ctc tcc cgc ctt ttt Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp Leu Ser Arg Leu Phe 430 435 440	4041
tgagacccag ctttcttgta caaagtgggtg ataacatcga taatcaacct ctggattaca	4101
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Warf Sequence.ST25.txt

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Leu

cca atg ctt aat cag tga ggc acc tat ctc agc gat ctg tct att tcg 6666
Pro Met Leu Asn Gln Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser
445 450 455

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Phe Ile His Ser Cys Leu Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr
460 465 470

gga ggg ctt acc atc tgg ccc cag tgc tgc aat gat acc gcg aga ccc 6762
Gly Gly Leu Thr Ile Trp Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro
475 480 485

acg ctc acc ggc tcc aga ttt atc agc aat aaa cca gcc agc cgg aag 6810
Thr Leu Thr Gly Ser Arg Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys
490 495 500 505

ggc cga gcg cag aag tgg tcc tgc aac ttt atc cgc ctc cat cca gtc 6858
Gly Arg Ala Gln Lys Trp Ser Cys Asn Phe Ile Arg Leu His Pro Val
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tat taa ttg ttg ccg gga agc tag agt aag tag ttc gcc agt taa tag 6906

Warf Sequence.ST25.txt

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agt tac atg atc ccc cat gtt gtg caa aaa agc ggt tag ctc ctt cgg Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly Leu Leu Arg	7050															
tcc tcc gat cgt tgt cag aag taa gtt ggc cgc agt gtt atc act cat Ser Ser Asp Arg Cys Gln Lys Val Gly Arg Ser Val Ile Thr His	7098															
ggt tat ggc agc act gca taa ttc tct tac tgt cat gcc atc cgt aag Gly Tyr Gly Ser Thr Ala Phe Ser Tyr Cys His Ala Ile Arg Lys	7146															
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ttc ttc ggg gcg aaa act ctc aag gat ctt acc gct gtt gag atc cag Phe Phe Gly Ala Lys Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln	7338															
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ttt cac cag cgt ttc tgg gtg agc aaa aac agg aag gca aaa tgc cgc Phe His Gln Arg Phe Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg	7434															
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warf Sequence.ST25.txt

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Thr Ala Thr Ile Asn Ser Ile Pro Ile Ser Glu Asp Tyr Ser Val Ala
20 25 30

Ser Ala Ala Leu Ser Ser Asp Gly Arg Ile Phe Thr Gly Val Asn Val
35 40 45

Tyr His Phe Thr Gly Gly Pro Cys Ala Glu Leu Val Val Leu Gly Thr
50 55 60

Ala Ala Ala Ala Ala Ala Gly Asn Leu Thr Cys Ile Val Ala Ile Gly
65 70 75 80

Asn Glu Asn Arg Gly Ile Leu Ser Pro Cys Gly Arg Cys Arg Gln Val
85 90 95

Leu Leu Asp Leu His Pro Gly Ile Lys Ala Ile Val Lys Asp Ser Asp
100 105 110

Gly Gln Pro Thr Ala Val Gly Ile Arg Glu Leu Leu Pro Ser Gly Tyr
115 120 125

Val Trp Glu Gly
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<212> PRT

<213> Artificial

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<223> Synthetic Construct

<400> 16

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1 5 10 15

Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
20 25 30

Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr Leu
35 40 45

warf Sequence.ST25.txt

Thr Cys Glu Thr His Arg Ile Asn Trp Thr Ala Asp Gly Arg Pro Cys
 50 55 60
 Gly Leu Asn Gly Thr Leu Phe Pro Arg Leu His Val Ser Glu Thr Arg
 65 70 75 80
 Pro Gln Gly Pro Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
 85 90 95
 Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
 100 105 110
 Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
 115 120 125
 Pro Ile Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
 130 135 140
 Pro Val Leu Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
 145 150 155 160
 Leu Leu Pro Ser Phe Asp Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
 165 170 175
 Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
 180 185 190
 Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
 195 200 205
 Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
 210 215 220
 Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
 225 230 235 240
 Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
 245 250 255
 Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
 260 265 270
 Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
 275 280 285
 Ile Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
 Page 20

290

295

Leu Ser Arg Leu Phe
305

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<211> 6

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 17

Leu Pro Met Leu Asn Gln
1 5

<210> 18

<211> 75

<212> PRT

<213> Artificial

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<223> Synthetic Construct

<400> 18

Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu
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Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
20 25 30

Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
35 40 45

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
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Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
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<213> Artificial

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<223> Synthetic Construct

<400> 19

Leu Leu Pro Gly Ser
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warf Sequence.ST25.txt

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<220>
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<400> 20

Phe Ala Gln Arg Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu
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 20 25 30

Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
 35 40

<210> 21
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<220>
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<400> 21

Leu Leu Arg Ser Ser Asp Arg Cys Gln Lys
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<210> 23
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 <212> PRT
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<220>
 <223> Synthetic Construct

<400> 23

Phe Ser Tyr Cys His Ala Ile Arg Lys Met Leu Phe Cys Asp Trp

1 5 15

<210> 24
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<212> PRT
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<220>
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<400> 24

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Leu Leu Pro Gly Val Asn Thr Gly
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<220>
<223> Synthetic Construct

<400> 25

Tyr Arg Ala Thr
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<220>
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<400> 26

Gln Asn Phe Lys Ser Ala His His Trp Lys Thr Phe Phe Gly Ala Lys
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Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr His
20 25 30

Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
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Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys
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Gly Asp Thr Glu Met Leu Asn Thr His
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warf Sequence.ST25.txt

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<212> DNA
<213> Artificial

<220>
<223> Engineered Sequence from virus and plasmid

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<223> 5' MoMuSVLTR

<220>
<221> CDS
<222> (1512)..(2306)
<223> neomycin resistance

<220>
<221> misc_feature
<222> (3023)..(3047)
<223> attB1

<220>
<221> CDS
<222> (3120)..(3590)
<223> trans-dominant BLV Rex (M4)

<220>
<221> misc_feature
<222> (3653)..(4282)
<223> attB2

<220>
<221> misc_signal
<222> (3690)..(4282)
<223> WPRE; woodchuck hepatitis virus post-transcriptional regulatory
      element

<220>
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<220>
<221> CDS
<222> (6217)..(7077)
<223> ampicillin resistance

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gatgagacag ctgagtgatg ggccaaacag gatatctgtg gtaagcagtt cctgccccgg      240
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warf Sequence.ST25.txt

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Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile	
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Gly Cys Ser Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro	
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Val Leu Phe Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln	
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Asp Glu Ala Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys	
65 70 75	
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warf Sequence.ST25.txt

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gcc gag aaa gta tcc atc atg gct gat gca atg cgg cgg ctg cat acg Ala Glu Lys Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr 110 115 120 125	1886
ctt gat ccg gct acc tgc cca ttc gac cac caa gcg aaa cat cgc atc Leu Asp Pro Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile 130 135 140	1934
gag cga gca cgt act cgg atg gaa gcc ggt ctt gtc gat cag gat gat Glu Arg Ala Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp 145 150 155	1982
ctg gac gaa gag cat cag ggg ctc gcg cca gcc gaa ctg ttc gcc agg Leu Asp Glu Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg 160 165 170	2030
ctc aag gcg cgc atg ccc gac ggc gag gat ctc gtc gtg acc cat ggc Leu Lys Ala Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly 175 180 185	2078
gat gcc tgc ttg ccg aat atc atg gtg gaa aat ggc cgc ttt tct gga Asp Ala Cys Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly 190 195 200 205	2126
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gac cgc ttc ctc gtg ctt tac ggt atc gcc gct ccc gat tcg cag cgc Asp Arg Phe Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg 240 245 250	2270
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warf Sequence.ST25.txt																		
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			Met	Pro	Lys	Lys	Arg	Arg	Ser	Arg	Arg	Arg						
			265											270				
cca	caa	ccg	atc	atc	aga	tgg	caa	gtg	ttg	ttg	gtt	ggg	ggc	ccc	act	3197		
Pro	Gln	Pro	Ile	Ile	Arg	Trp	Gln	Val	Leu	Leu	Val	Gly	Gly	Pro	Thr			
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ctc	tac	atg	cct	gcc	cgg	ccc	tgg	ttt	tgt	cca	atg	atg	tca	cca	tcg	3245		
Leu	Tyr	Met	Pro	Ala	Arg	Pro	Trp	Phe	Cys	Pro	Met	Met	Ser	Pro	Ser			
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gga	tcg	aca	cca	cgc	tca	cct	gcg	aga	ccc	acc	gta	tca	act	gga	ccg	3341		
Gly	Ser	Thr	Pro	Arg	Ser	Pro	Ala	Arg	Pro	Thr	Val	Ser	Thr	Gly	Pro			
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ccg	atg	gac	gac	ctt	gcg	gcc	tca	atg	gaa	cgt	tgt	tcc	ctc	gac	tgc	3389		
Pro	Met	Asp	Asp	Leu	Ala	Ala	Ser	Met	Glu	Arg	Cys	Ser	Leu	Asp	Cys			
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Met	Ser	Pro	Arg	Pro	Ala	Pro	Lys	Gly	Pro	Asp	Asp	Ser	Gly	Ser	Thr			
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gcc	ccc	ttc	cgg	ccg	ttc	gcg	ctc	agc	ccg	gcc	cgg	tta	gat	ctt	ccc	3485		
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Thr	Thr																	
				420														
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Warf Sequence.ST25.txt

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Warf Sequence.ST25.txt

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tgacag tta cca atg ctt aat cag tga ggc acc tat ctc agc gat ctg Leu Pro Met Leu Asn Gln Gly Thr Tyr Leu Ser Asp Leu	6258
	425 430
tct att tcg ttc atc cat agt tgc ctg act ccc cgt cgt gta gat aac Ser Ile Ser Phe Ile His Ser Cys Leu Thr Pro Arg Arg Val Asp Asn	6306
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	485 490 495
cat cca gtc tat taa ttg ttg ccg gga agc tag agt aag tag ttc gcc His Pro Val Tyr Leu Leu Pro Gly Ser Ser Lys Phe Ala	6498
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	545 550 555
ctc ctt cgg tcc tcc gat cgt tgt cag aag taa gtt ggc cgc agt gtt Leu Leu Arg Ser Ser Asp Arg Cys Gln Lys Val Val Gly Arg Ser Val	6690
	560 565 570
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	590 595 600
ctg aga ata gtg tat gcg gcg acc gag ttg ctc ttg ccc ggc gtc aac Leu Arg Ile Val Tyr Ala Ala Thr Glu Leu Leu Leu Pro Gly Val Asn	6834
	605 610 615

warf Sequence.ST25.txt

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Thr Gly Tyr Arg Ala Thr Gln Asn Phe Lys Ser Ala His His 630
620 625

tgg aaa acg ttc ttc ggg gcg aaa act ctc aag gat ctt acc gct gtt 6930
Trp Lys Thr Phe Phe Gly Ala Lys Thr Leu Lys Asp Leu Thr Ala Val 645
635 640

gag atc cag ttc gat gta acc cac tcg tgc acc caa ctg atc ttc agc 6978
Glu Ile Gln Phe Asp Val Thr His Ser Cys Thr Gln Leu Ile Phe Ser 660
650 655

atc ttt tac ttt cac cag cgt ttc tgg gtg agc aaa aac agg aag gca 7026
Ile Phe Tyr Phe His Gln Arg Phe Trp Val Ser Lys Asn Arg Lys Ala 675
665 670

aaa tgc cgc aaa aaa ggg aat aag ggc gac acg gaa atg ttg aat act 7074
Lys Cys Arg Lys Lys Gly Asn Lys Gly Asp Thr Glu Met Leu Asn Thr 690
680 685

cat actcttcctt ttccaatatt attgaagcat ttatcagggt tattgtctca 7127
His 695

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ttccccgaaa agtgccacct gacgtctaag aaaccattat tatcatgaca ttaacctata 7247

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 <213> Artificial

<220>
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<400> 28

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Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
           20           25           30

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Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
           35           40           45

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Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
50           55           60

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warf Sequence.ST25.txt

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65 70 75 80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
85 90 95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
100 105 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
115 120 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
130 135 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145 150 155 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
165 170 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
180 185 190

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
195 200 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
210 215 220

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
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Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
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Tyr Arg Leu Leu Asp Glu Phe Phe
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Warf Sequence.ST25.txt

Met Pro Lys Lys Arg Arg Ser Arg Arg Arg Pro Gln Pro Ile Ile Arg
1 5 10 15

Trp Gln Val Leu Leu Val Gly Gly Pro Thr Leu Tyr Met Pro Ala Arg
20 25 30

Pro Trp Phe Cys Pro Met Met Ser Pro Ser Met Pro Gly Ala Pro Ser
35 40 45

Ala Gly Pro Met Ser Asp Ser Asn Ser Lys Gly Ser Thr Pro Arg Ser
50 55 60

Pro Ala Arg Pro Thr Val Ser Thr Gly Pro Pro Met Asp Asp Leu Ala
65 70 75 80

Ala Ser Met Glu Arg Cys Ser Leu Asp Cys Met Ser Pro Arg Pro Ala
85 90 95

Pro Lys Gly Pro Asp Asp Ser Gly Ser Thr Ala Pro Phe Arg Pro Phe
100 105 110

Ala Leu Ser Pro Ala Arg Leu Asp Leu Pro Pro Ser Ser Gly Pro Pro
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Ser Ser Pro Thr Asn Ala Asn Cys Pro Arg Pro Leu Ala Thr Val Ala
130 135 140

Pro Leu Ser Gly Thr Ala Phe Phe Pro Gly Thr Thr
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warf Sequence.ST25.txt

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Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
20 25 30

Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
35 40 45

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
50 55 60

Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
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<400> 32

Leu Leu Pro Gly Ser
1 5

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Phe Ala Gln Arg Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu
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Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala
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Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
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<210> 34
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<400> 35

Val Gly Arg Ser Val Ile Thr His Gly Tyr Gly Ser Thr Ala
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<220>

<223> Synthetic Construct

<400> 37

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Leu Leu Pro Gly Val Asn Thr Gly
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<211> 4

<212> PRT

<213> Artificial

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warf Sequence.ST25.txt

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Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr His
20 25 30

Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
35 40 45

Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys
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Gly Asp Thr Glu Met Leu Asn Thr His
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warf Sequence.ST25.txt

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 <223> EYFP; enhanced yellow florescent protein

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warf Sequence.ST25.txt

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Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly	10 15 20
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Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala Ala Val Phe	25 30 35
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Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu	40 45 50
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Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala Ala Arg Leu Ser Trp	55 60 65
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Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val Leu Asp Val Val Thr	70 75 80 85
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Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu Val Pro Gly Gln Asp	90 95 100
ctc ctg tca tct cac ctt gct cct gcc gag aaa gta tcc atc atg gct	2010
Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys Val Ser Ile Met Ala	105 110 115
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Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro Ala Thr Cys Pro Phe	120 125 130
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Asp His Gln Ala Lys His Arg Ile Glu Arg Ala Arg Thr Arg Met Glu	135 140 145
gcc ggt ctt gtc gat cag gat gat ctg gac gaa gag cat cag ggg ctc	2154
Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu Glu His Gln Gly Leu	150 155 160 165
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Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala Arg Met Pro Asp Gly	170 175 180
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Warf Sequence.ST25.txt

185	190	195	
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ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp 310 315 320			3409
ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc gcc cgc			3457

Warf Sequence.ST25.txt

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Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	
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tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	3601
Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	
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cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	3649
Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	
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ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	3697
Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	
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Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	
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Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	
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acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	3841
Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	
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atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	3937
Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	
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Asp	Glu	Leu	Tyr	Lys												
	500															
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Warf Sequence.ST25.txt

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                                Leu Pro Met Leu Asn
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cag tga ggc acc tat ctc agc gat ctg tct att tcg ttc atc cat agt 6007
Gln   Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser
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tgc ctg act ccc cgt cgt gta gat aac tac gat acg gga ggg ctt acc 6055
Cys Leu Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr
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atc tgg ccc cag tgc tgc aat gat acc gcg aga ccc acg ctc acc ggc 6103
Ile Trp Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly
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warf Sequence.ST25.txt

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ccg gga agc tag agt aag tag ttc gcc agt taa tag ttt gcg caa cgt Pro Gly Ser Ser Lys Phe Ala Ser Phe Ala Gln Arg 590 595	6247
tgt tgc cat tgc tgc agg cat cgt ggt gtc acg ctc gtc gtt tgg tat Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu Val Val Trp Tyr 600 605 610	6295
ggc ttc att cag ctc cgg ttc cca acg atc aag gcg agt tac atg atc Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala Ser Tyr Met Ile 615 620 630	6343
ccc cat gtt gtg caa aaa agc ggt tag ctc ctt cgg tcc tcc gat cgt Pro His Val Val Gln Lys Ser Gly Leu Leu Arg Ser Ser Asp Arg 635 640 645	6391
tgt cag aag taa gtt ggc cgc agt gtt atc act cat ggt tat ggc agc Cys Gln Lys Val Gly Arg Ser Val Ile Thr His Gly Tyr Gly Ser 650 655 660	6439
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acc gag ttg ctc ttg ccc ggc gtc aac acg gga taa tac cgc gcc aca Thr Glu Leu Leu Leu Pro Gly Val Asn Thr Gly Tyr Arg Ala Thr 695 700 705	6583
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aag ggc gac acg gaa atg ttg aat act cat actcttcctt tttcaatatt Lys Gly Asp Thr Glu Met Leu Asn Thr His 770 775	6825
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Warf Sequence.ST25.txt

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 ttcaa 7010

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Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
 35 40 45

Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
 50 55 60

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
 65 70 75 80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
 85 90 95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
 100 105 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
 115 120 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
 130 135 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
 145 150 155 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
 165 170 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
 180 185 190

warf Sequence.ST25.txt

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
195 200 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
210 215 220

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225 230 235 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
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Tyr Arg Leu Leu Asp Glu Phe Phe
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
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Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

warf Sequence.ST25.txt

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu
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Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
20 25 30

Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
35 40 45

warf Sequence.ST25.txt

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
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Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
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<400> 45

Leu Leu Pro Gly Ser
1 5

<210> 46
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<220>
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<400> 46

Phe Ala Gln Arg Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu
1 5 10 15

Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala
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Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
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warf Sequence.ST25.txt

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<211> 15

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<211> 4

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Tyr Arg Ala Thr
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<211> 73

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warf Sequence.ST25.txt

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Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
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Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys
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Gly Asp Thr Glu Met Leu Asn Thr His
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<211> 7121

<212> DNA

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<223> Engineered Sequence from virus and plasmid

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<221> LTR

<222> (149)..(737)

<223> 5' MoMuSVLTR

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<221> CDS

<222> (1660)..(2454)

<223> neomycin resistance

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<221> promoter

<222> (2806)..(3261)

<223> HIV promoter

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<221> misc_feature

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<222> (3347)..(4066)

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<221> misc_feature

<222> (4091)..(4115)

<223> attB2

warf Sequence.ST25.txt

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 <223> 3' MoMuLVLTR

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 <223> ampicillin resistance

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cgtctgaatt tttgctttcg gtttggaacc gaagccgcgc gtcttgtctg ctgcagcgct     1140
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accctaagcc tccgcctcct cttcctccat ccgccccgtc tctccccctt gaacctctc     1560
    
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Warf Sequence.ST25.txt

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gga ttg cac gca ggt tct ccg gcc gct tgg gtg gag agg cta ttc ggc Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly 10 15 20	1722
tat gac tgg gca caa cag aca atc ggc tgc tct gat gcc gcc gtg ttc Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala Ala Val Phe 25 30 35	1770
cgg ctg tca gcg cag ggg cgc ccg gtt ctt ttt gtc aag acc gac ctg Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu 40 45 50	1818
tcc ggt gcc ctg aat gaa ctg cag gac gag gca gcg cgg cta tcg tgg Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala Ala Arg Leu Ser Trp 55 60 65	1866
ctg gcc acg acg ggc gtt cct tgc gca gct gtg ctc gac gtt gtc act Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val Leu Asp Val Val Thr 70 75 80 85	1914
gaa gcg gga agg gac tgg ctg cta ttg ggc gaa gtg ccg ggg cag gat Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu Val Pro Gly Gln Asp 90 95 100	1962
ctc ctg tca tct cac ctt gct cct gcc gag aaa gta tcc atc atg gct Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys Val Ser Ile Met Ala 105 110 115	2010
gat gca atg cgg cgg ctg cat acg ctt gat ccg gct acc tgc cca ttc Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro Ala Thr Cys Pro Phe 120 125 130	2058
gac cac caa gcg aaa cat cgc atc gag cga gca cgt act cgg atg gaa Asp His Gln Ala Lys His Arg Ile Glu Arg Ala Arg Thr Arg Met Glu 135 140 145	2106
gcc ggt ctt gtc gat cag gat gat ctg gac gaa gag cat cag ggg ctc Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu Glu His Gln Gly Leu 150 155 160 165	2154
gcg cca gcc gaa ctg ttc gcc agg ctc aag gcg cgc atg ccc gac ggc Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala Arg Met Pro Asp Gly 170 175 180	2202
gag gat ctc gtc gtg acc cat ggc gat gcc tgc ttg ccg aat atc atg Glu Asp Leu Val Val Thr His Gly Asp Ala Cys Leu Pro Asn Ile Met 185 190 195	2250
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gaa gag ctt ggc ggc gaa tgg gct gac cgc ttc ctc gtg ctt tac ggt	2394

warf Sequence.ST25.txt

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Ile	Ala	Ala	Pro	Asp	Ser	Gln	Arg	Ile	Ala	Phe	Tyr	Arg	Leu	Leu	Asp		
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gag	ttc	ttc	tga	gcgggactct	gggggttcgaa	atgaccgacc	aagcgacgcc									2494	
Glu	Phe	Phe															
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Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu		
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aag	ttc	atc	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	3529	
Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu		
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cac	atg	aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	3625	
His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr		
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Warf Sequence.ST25.txt

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ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys 390 395 400 405	3769
ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc gac aag Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys 410 415 420	3817
cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu 425 430 435	3865
gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile 440 445 450	3913
ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln 455 460 465	3961
tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu 470 475 480 485	4009
ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu 490 495 500	4057
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warf Sequence.ST25.txt

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acc tat ctg agc gat ctg tct att tcg ttc atc cat agt tgc ctg act	6127
Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu Thr	515 520 525
ccc cgt cgt gta gat aac tac gat acg gga ggg ctt acc atc tgg ccc	6175
Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp Pro	530 535 540
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Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg Phe	545 550 555
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Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp Ser	560 565 570
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Cys Asn Phe Ile Arg Leu His Pro Val Tyr Leu Leu Pro Gly Ser	

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warf Sequence.ST25.txt

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<213> Artificial

<220>
<223> Synthetic Construct

<400> 54

Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
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Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
20 25 30

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
35 40 45

Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
50 55 60

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65 70 75 80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
85 90 95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
100 105 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
115 120 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
130 135 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145 150 155 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
165 170 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
180 185 190

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
195 200 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
210 215 220

Warf Sequence.ST25.txt

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
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Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
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Tyr Arg Leu Leu Asp Glu Phe Phe
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<210> 55
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<220>
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<400> 55

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

warf Sequence.ST25.txt

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
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Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

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Leu Pro Met Leu Asn Gln
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Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
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Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
35 40 45

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
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Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
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warf Sequence.ST25.txt

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Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala
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Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
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warf Sequence.ST25.txt

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Leu Leu Pro Gly Val Asn Thr Gly
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Gln Asn Phe Lys Ser Ala His His Trp Lys Thr Phe Phe Gly Ala Lys
 1 5 10 15

Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr His
 Page 58

Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
35 40 45
Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys
50 55 60
Gly Asp Thr Glu Met Leu Asn Thr His
65 70